

C. Jeffers
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/714,602

DATE: 11/14/2003

TIME: 13:45:35

Input Set : N:\Crf3\RULE60\09714602.raw.txt

Output Set: N:\CRF4\11142003\I714602.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 4 (i) APPLICANT: David William Holden
 5 (ii) TITLE OF INVENTION: Identification of Genes
 6 (iii) NUMBER OF SEQUENCES: 501
 7 (iv) CORRESPONDENCE ADDRESS:
 8 (A) ADDRESSEE: Patrea L. Pabst
 9 (B) STREET: 2800 One Atlantic Center
 10 1201 West Peachtree Street
 11 (C) CITY: Atlanta
 12 (D) STATE: Georgia
 13 (E) COUNTRY: USA
 14 (F) ZIP: 30309-3450
 15 (v) COMPUTER READABLE FORM:
 16 (A) MEDIUM TYPE: Floppy disk
 17 (B) COMPUTER: IBM PC compatible
 18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 19 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 20 (vi) CURRENT APPLICATION DATA:
 C--> 21 (A) APPLICATION NUMBER: US/09/714,602
 C--> 22 (B) FILING DATE: 16-Nov-2000
 W--> 31 (C) CLASSIFICATION: 435
 28 (vii) PRIOR APPLICATION DATA:
 25 (A) APPLICATION NUMBER: US/08/871,355A
 26 (B) FILING DATE: 09-JUN-1997
 29 (A) APPLICATION NUMBER: PCT/GB95/02875
 30 (B) FILING DATE: 11-DEC-1995
 32 (viii) ATTORNEY/AGENT INFORMATION:
 33 (A) NAME: Pabst, Patrea L.
 34 (B) REGISTRATION NUMBER: 31,284
 35 (C) REFERENCE/DOCKET NUMBER: RPMS 101 CON
 36 (ix) TELECOMMUNICATION INFORMATION:
 37 (A) TELEPHONE: (404) 873-8794
 38 (B) TELEFAX: (404) 873-8795
 40 (2) INFORMATION FOR SEQ ID NO: 1:
 41 (i) SEQUENCE CHARACTERISTICS:
 42 (A) LENGTH: 89 base pairs
 43 (B) TYPE: nucleic acid
 44 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear
 46 (ii) MOLECULE TYPE: cDNA
 47 (iii) HYPOTHETICAL: NO
 C--> 48 (iv) ANTI-SENSE: NO

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```

49      (vi) ORIGINAL SOURCE:
50          (A) ORGANISM: Synthetic oligonucleotide
51      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
52      CTAGGTACCT ACAACCTCAA GCTTNKNKNK NKNKNKNKNK NKNKNKNKNK NKNKNKNKNK      60
53      NKNKAAGCTT GGTTAGAATG GGTACCATG      89
54      (2) INFORMATION FOR SEQ ID NO: 2:
55          (i) SEQUENCE CHARACTERISTICS:
56              (A) LENGTH: 18 base pairs
57              (B) TYPE: nucleic acid
58              (C) STRANDEDNESS: single
59              (D) TOPOLOGY: linear
60          (ii) MOLECULE TYPE: cDNA
61          (iii) HYPOTHETICAL: NO
C--> 62      (iv) ANTI-SENSE: NO
63      (vi) ORIGINAL SOURCE:
64          (A) ORGANISM: Synthetic oligonucleotide
65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
66      TACCTACAAC CTCAAGCT      18
67      (2) INFORMATION FOR SEQ ID NO: 3:
68          (i) SEQUENCE CHARACTERISTICS:
69              (A) LENGTH: 18 base pairs
70              (B) TYPE: nucleic acid
71              (C) STRANDEDNESS: single
72              (D) TOPOLOGY: linear
73          (ii) MOLECULE TYPE: cDNA
74          (iii) HYPOTHETICAL: NO
C--> 75      (iv) ANTI-SENSE: NO
76      (vi) ORIGINAL SOURCE:
77          (A) ORGANISM: Synthetic oligonucleotide
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
79      CATGGTACCC ATTCTAAC      18
80      (2) INFORMATION FOR SEQ ID NO: 4:
81          (i) SEQUENCE CHARACTERISTICS:
82              (A) LENGTH: 18 base pairs
83              (B) TYPE: nucleic acid
84              (C) STRANDEDNESS: single
85              (D) TOPOLOGY: linear
86          (ii) MOLECULE TYPE: cDNA
87          (iii) HYPOTHETICAL: NO
C--> 88      (iv) ANTI-SENSE: NO
89      (vi) ORIGINAL SOURCE:
90          (A) ORGANISM: Synthetic oligonucleotide
91      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
92      TACCCATTCT AACCAAGC      18
93      (2) INFORMATION FOR SEQ ID NO: 5:
94          (i) SEQUENCE CHARACTERISTICS:
95              (A) LENGTH: 18 base pairs
96              (B) TYPE: nucleic acid
97              (C) STRANDEDNESS: single

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111         (D) TOPOLOGY: linear
112     (ii) MOLECULE TYPE: cDNA
113     (iii) HYPOTHETICAL: NO
C--> 114     (iv) ANTI-SENSE: NO
115     (vi) ORIGINAL SOURCE:
116         (A) ORGANISM: Synthetic oligonucleotide
118     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
120 CTAGGTACCT ACAACCTC                                     18
122 (2) INFORMATION FOR SEQ ID NO: 6:
123     (i) SEQUENCE CHARACTERISTICS:
124         (A) LENGTH: 20 base pairs
125         (B) TYPE: nucleic acid
126         (C) STRANDEDNESS: single
127         (D) TOPOLOGY: linear
128     (ii) MOLECULE TYPE: cDNA
129     (iii) HYPOTHETICAL: NO
C--> 130     (iv) ANTI-SENSE: NO
131     (vi) ORIGINAL SOURCE:
132         (A) ORGANISM: Synthetic oligonucleotide
134     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
136 CCTAGGCGGC CAGATCTGAT                                     20
138 (2) INFORMATION FOR SEQ ID NO: 7:
139     (i) SEQUENCE CHARACTERISTICS:
140         (A) LENGTH: 21 base pairs
141         (B) TYPE: nucleic acid
142         (C) STRANDEDNESS: single
143         (D) TOPOLOGY: linear
144     (ii) MOLECULE TYPE: cDNA
145     (iii) HYPOTHETICAL: NO
C--> 146     (iv) ANTI-SENSE: NO
147     (vi) ORIGINAL SOURCE:
148         (A) ORGANISM: Synthetic oligonucleotide
150     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
152 GCACTTGTGT ATAAGAGTCA G                                     21
154 (2) INFORMATION FOR SEQ ID NO: 8:
155     (i) SEQUENCE CHARACTERISTICS:
156         (A) LENGTH: 300 base pairs
157         (B) TYPE: nucleic acid
158         (C) STRANDEDNESS: double
159         (D) TOPOLOGY: linear
160     (ii) MOLECULE TYPE: DNA (genomic)
161     (iii) HYPOTHETICAL: NO
C--> 162     (iv) ANTI-SENSE: NO
163     (vi) ORIGINAL SOURCE:
164         (A) ORGANISM: Partial sequence of Salmonella typhimurium
165                 virulence gene
167     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
169 GGTCTTAATG TACGGGCATG GTCTGCATCG ATAACTCCGG CACGCAAATC GCCATCGATA      60
171 CTCATTTGTT TGGCTGGCAT CCCATCAAGC GAGAAACGTG CGCTAACTTC CGCCACCCTC      120

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173 TCGATACCTT TTGTAATGAC AATAAATTGC ACGATAGTAA TGATGGTAAA TACGACCAAC      180
175 CCAACGGTGA GATTTCTCTC TACGACAAAC TTACCGAAAG CATCCACAAA TATTACCGGC      240
177 ATTATGTTGT AACAGTACCC AGCCGTGATG TGCTGATTGG GGAGTTAACA ACCGATTAT      300
179 (2) INFORMATION FOR SEQ ID NO: 9:
180     (i) SEQUENCE CHARACTERISTICS:
181         (A) LENGTH: 300 base pairs
182         (B) TYPE: nucleic acid
183         (C) STRANDEDNESS: double
184         (D) TOPOLOGY: linear
185     (ii) MOLECULE TYPE: DNA (genomic)
186     (iii) HYPOTHETICAL: NO
C--> 187     (iv) ANTI-SENSE: NO
188     (vi) ORIGINAL SOURCE:
189         (A) ORGANISM: Partial sequence of Salmonella typhimurium
190                 virulence gene
192     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
194 GCGCGGACGC TAGTGTGGTG GGTGACAGCC AGACGTTACC GAACGGGATG GGGCAGATCT      60
196 GTTGGCTTAC AAAAGACATG GCCCATAAGG CGCAAGGTTT TGGGACTGGA CGTTTTTCGCG      120
198 GGCAGACAAC GTATCTCTGT CTTATTAAAA TGTGTCCTGC TTCGGCATAT GTATCGAACC      180
200 CTCGGAGCAA AGTCGTTTGG GCGCAGAATT AGTACGTTTG GGTCGGTTGC TGTTATTCCT      240
202 TGGGCTCGGA AAAAGAGTGC CAGCGTGAAG GAGTGGGATT TGGCAGACTG GCCGCCTAAT      300
204 (2) INFORMATION FOR SEQ ID NO: 10:
205     (i) SEQUENCE CHARACTERISTICS:
206         (A) LENGTH: 300 base pairs
207         (B) TYPE: nucleic acid
208         (C) STRANDEDNESS: double
209         (D) TOPOLOGY: linear
210     (ii) MOLECULE TYPE: DNA (genomic)
211     (iii) HYPOTHETICAL: NO
C--> 212     (iv) ANTI-SENSE: NO
213     (vi) ORIGINAL SOURCE:
214         (A) ORGANISM: Partial sequence of Salmonella typhimurium
215                 virulence gene
217     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
219 CACTATAGGG AAAGCTTGCA TGCCTGCAGG TCGACTCTAG AGGATCTACT AGTCATATGG      60
221 ATTGCACTTG TGTATAAGAG TCAGGATTAG AGGACATGCG CCGGGAACCA TACTATCTTT      120
223 TTCCGGTGCT TCGACGCCAT TTGCGGAAAC CACAGACTTT TTGCGGCGAA TGAGGATAAT      180
225 TGGCAATGCT AACAACGCTG AAAAGAAAGC GAGAGTGATA AAAGGAAAGC CAGGAATTAA      240
227 AGCGAGGAGC ATTAAAACCA CAGCGGCTAA TATGAGCGAC TGAGGTTGTC TGGCAATTTG      300
229 (2) INFORMATION FOR SEQ ID NO: 11:
230     (i) SEQUENCE CHARACTERISTICS:
231         (A) LENGTH: 300 base pairs
232         (B) TYPE: nucleic acid
233         (C) STRANDEDNESS: double
234         (D) TOPOLOGY: linear
235     (ii) MOLECULE TYPE: DNA (genomic)
236     (iii) HYPOTHETICAL: NO
C--> 237     (iv) ANTI-SENSE: NO
238     (vi) ORIGINAL SOURCE:

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Output Set: N:\CRF4\11142003\I714602.raw

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239      (A) ORGANISM: Partial sequence of Salmonella typhimurium
240                      virulence gene
242      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
244 TGCAGGCCGA CTCTAGAGGA TCCCCGGGTA CCGGTAATTT CTTTAACCTC GCATCCCGGT      60
246 GGATGAAAGG ATATTCTGGC TGCCTAAGTA ATGAATGAAC CGCCCAGTAG ATAAAATATT      120
248 GAAAGTGATA ACCTGATGTT TTAATAACGA TGCAGGATAT ACATATAACA TGCTGGCATC      180
250 AAACCAGGTA AGCAAATCAT ATTGTGCTGC CAGGTTATTC AACTATCGA CCGGTGGTCC      240
252 AGGCGGGAAT TTTTCCACTA AATGTAGGTG GGATCAATGG GCTAATTGGT ATAGGCGGAT      300
254 (2) INFORMATION FOR SEQ ID NO: 12:
255      (i) SEQUENCE CHARACTERISTICS:
256          (A) LENGTH: 324 base pairs
257          (B) TYPE: nucleic acid
258          (C) STRANDEDNESS: double
259          (D) TOPOLOGY: linear
260      (ii) MOLECULE TYPE: DNA (genomic)
261      (iii) HYPOTHETICAL: NO
C--> 262      (iv) ANTI-SENSE: NO
263      (vi) ORIGINAL SOURCE:
264          (A) ORGANISM: Partial sequence of Salmonella typhimurium
265                      virulence gene
267      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
269 CCTGTGATTC CGGATGAAAT AGCTTTTACG AAAGCTGTCA GACNTGCTGA AGAATACGCT      60
271 GCAAATGGTA AGCTTGTAAC TTTTGGGTAT TGTTCCAACG CATGCTGAAA CGGGTTATGG      120
273 ATATATTCGT CGCGGTGAGT TGATAGGAAA TGACGCTTAT GCAGTGGCTG AATTTGTGGA      180
275 GAAACCGGAT ATCGATACCG CCCGTGACTA TTTCAAATCA GGGGAAATAT TACTGGCCTA      240
277 GCGGCGATGT TTTTATTTTCG CGCAAAGCCC TTATTTAAAC GAATTAAACG TATCTATCAC      300
279 CCCCAAATTC ATACAGCTTG TGAA      324
281 (2) INFORMATION FOR SEQ ID NO: 13:
282      (i) SEQUENCE CHARACTERISTICS:
283          (A) LENGTH: 292 base pairs
284          (B) TYPE: nucleic acid
285          (C) STRANDEDNESS: double
286          (D) TOPOLOGY: linear
287      (ii) MOLECULE TYPE: DNA (genomic)
288      (iii) HYPOTHETICAL: NO
C--> 289      (iv) ANTI-SENSE: NO
290      (vi) ORIGINAL SOURCE:
291          (A) ORGANISM: Partial sequence of Salmonella typhimurium
292                      virulence gene
294      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
296 TTACTAAACA GGGCCCCGGA CCATGTAAAC ACCACGCTTG CCAACACTAA AAAACGATGC      60
298 TTGCCGTAAA AAAATTGAAC GTTATTTACT TAATACGCCT ATTTTATTTA CATTATGCAC      120
300 TGACAGAGGG TGAGGATTAA ATGGATAATA TTGATAATAA GTATACTCCA CAGCTATGTA      180
302 AAATTTTGGG GGCTATATCG GATTTGGTTG TTTTAAATTT AGCCTTATGG CTTTCACTAG      240
304 GATGTGTCTA TTTTTTTTGT GGTCAAGCAC AGAGATTTAT TCCCCAACCA CC      292
306 (2) INFORMATION FOR SEQ ID NO: 14:
307      (i) SEQUENCE CHARACTERISTICS:
308          (A) LENGTH: 300 base pairs
309          (B) TYPE: nucleic acid

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/714,602

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Output Set: N:\CRF4\11142003\I714602.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 25,27,29,31,33,35,37,39,41,43,45,47,49,51,53,55,57,59,61,63
Seq#:12; N Pos. 44
Seq#:37; N Pos. 3566
Seq#:38; N Pos. 87,97,106,107,110,111,114,115,116,304,1131,1165,1203,1213
Seq#:38; N Pos. 1239,1302,1506,1507,1690,1691,1692,1703,1704,1705,1738,1756
Seq#:38; N Pos. 1790,1849,1850,2326,2505,2744,2745,2746,2747,2748,2749,2750
Seq#:38; N Pos. 2751,2752,2753,2754,2755,2756,2757,2758,2759,2760,2761,2762
Seq#:38; N Pos. 2763,2764,2765,2766,2767,2768,2801,3025,3068,3145,3305,3306
Seq#:38; N Pos. 3307,3308,3309,3310,3611,4449,4737,4816,4817,5157,5158,5159
Seq#:38; N Pos. 5237,5238,5240,5605,5648,5649
Seq#:39; N Pos. 112
Seq#:89; Xaa Pos.75
Seq#:153; Xaa Pos.1
Seq#:231; Xaa Pos.3
Seq#:319; Xaa Pos.64
Seq#:393; Xaa Pos.46
Seq#:457; Xaa Pos.230

VERIFICATION SUMMARY

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Input Set : N:\Crif3\RULE60\09714602.raw.txt

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L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:31 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:48 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:66 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:82 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:98 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:114 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:130 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:146 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:162 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:187 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:212 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:237 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:262 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:289 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:314 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:339 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:364 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:387 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:414 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:439 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:464 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:489 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:514 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:541 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:566 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:593 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:618 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:645 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:670 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:695 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:720 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:745 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:770 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:795 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:820 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:847 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:872 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:897 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1360 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1566 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1584 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1600 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1618 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1633 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1649 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]

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L:2417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89 after pos.:64
L:3615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:153 after pos.:0
L:4972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:231 after pos.:0
L:6449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:319 after pos.:48
L:7752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:393 after pos.:32
L:8932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:457 after pos.:224